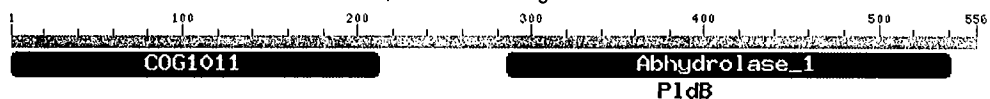


BLAST Basic Local Alignment Search ToolJob Title: human soluble epoxide hydrolase BLAST

Show Conserved Domains

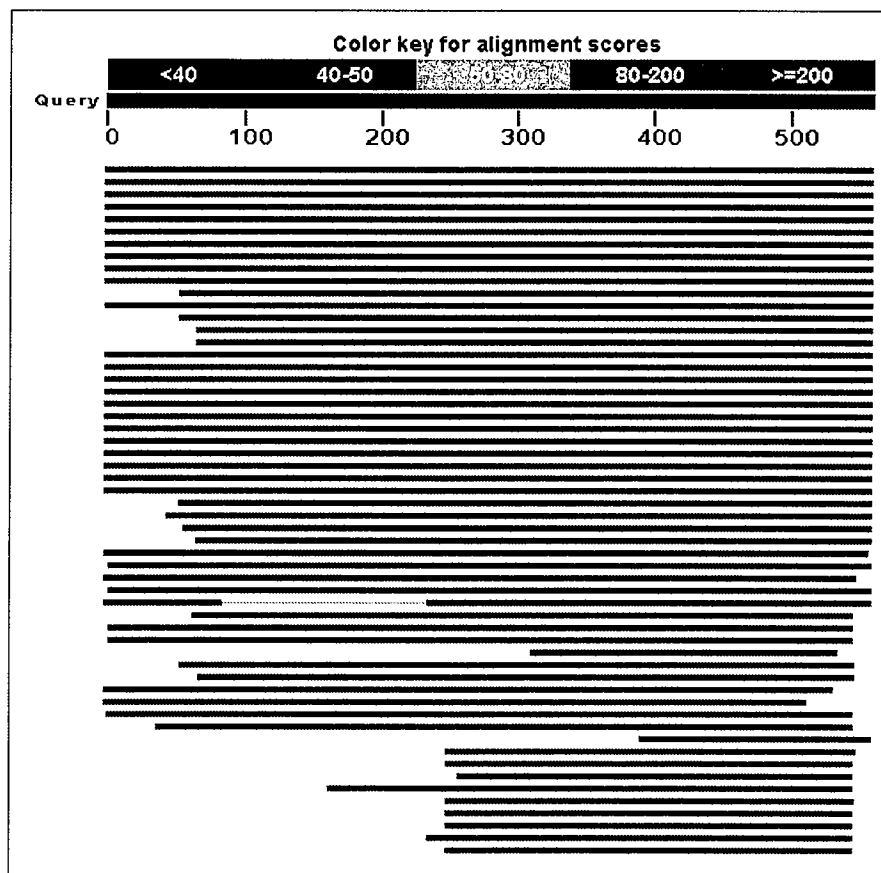
Putative conserved domains have been detected, click on the image below for detailed results.

**BLASTP 2.2.18 (Mar-02-2008)**

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402. Reference for compositional score matrix adjustment: Altschul, Stephen F., John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109. RID: 19UBW5CM014 **Database:** All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects 6,470,629 sequences; 2,208,486,882 total letters

Query= Length=556

Distribution of 101 Blast Hits on the Query Sequence



Distance tree of results **NEW**

Score

E

Sequences producing significant alignments:

(Bits) Value

gb AA014968.1 AF033336_1 soluble epoxide hydrolase [Homo sapi...	1157	0.0	G
gb AA014968.1 AF033336_1 Homo sapiens epoxide hydrolase 2, cytoplasmic ...	1151	0.0	
ref NP_001070.2 epoxide hydrolase 2, cytoplasmic [Homo sapie...	1150	0.0	UG
gb AA014967.1 AF233335_1 soluble epoxide hydrolase [Homo sapi...	1149	0.0	G
ref XP_001163779.1 PREDICTED: epoxide hydrolase 2, cytoplasm...	1141	0.0	UG
gb EAW63547.1 epoxide hydrolase 2, cytoplasmic, isoform CRA_...	1140	0.0	G
gb AAA02756.1 cytosolic epoxide hydrolase	1139	0.0	G
ref XP_001163855.1 PREDICTED: epoxide hydrolase 2, cytoplasm...	1126	0.0	G
ref XP_001099474.1 PREDICTED: similar to epoxide hydrolase 2...	1083	0.0	UG
ref XP_001163855.1 PREDICTED: epoxide hydrolase 2, cytoplasm...	1076	0.0	G
gb EAW63547.1 epoxide hydrolase 2, cytoplasmic, isoform CRA_...	1045	0.0	G
ref XP_001163855.1 PREDICTED: epoxide hydrolase 2, cytoplasm...	1040	0.0	UG
ref XP_001163857.1 PREDICTED: epoxide hydrolase 2, cytoplasm...	1036	0.0	UG
gb EAW63551.1 epoxide hydrolase 2, cytoplasmic, isoform CRA_...	1019	0.0	G
ref XP_001163855.1 PREDICTED: epoxide hydrolase 2, cytoplasm...	1011	0.0	UG
ref XP_534560.1 PREDICTED: similar to epoxide hydrolase 2, c...	931	0.0	UG
ref XP_857471.1 PREDICTED: similar to epoxide hydrolase 2, c...	930	0.0	UG
ref XP_001402725.1 PREDICTED: similar to soluble epoxide hyd...	929	0.0	UG
ref NP_001001641.1 soluble epoxide hydrolase [Sus scrofa] >s...	924	0.0	UG
ref XP_857554.1 PREDICTED: similar to epoxide hydrolase 2, c...	919	0.0	UG
ref XP_857430.1 PREDICTED: similar to epoxide hydrolase 2, c...	912	0.0	UG
ref NP_001069002.1 epoxide hydrolase 2, cytoplasmic [Bos tau...	902	0.0	UG
emb CAA85471.1 Epoxide Hydrolase [Mus musculus]	877	0.0	G
ref NP_031966.2 epoxide hydrolase 2, cytoplasmic [Mus muscul...	875	0.0	UG
dbj BAE25172.1 unnamed protein product [Mus musculus]	874	0.0	G
ref NP_076225.1 epoxide hydrolase 2, cytoplasmic [Rattus nor...	870	0.0	UG
gb AAH89732.1 Epoxide hydrolase 2, cytoplasmic [Rattus norve...	865	0.0	G
gb E0136006.1 epoxide hydrolase 2, cytoplasmic, isoform CRA_...	814	0.0	G
gb E0136377.1 epoxide hydrolase 2, cytoplasmic, isoform CRA_...	811	0.0	G
gb AAM28338.1 ovary-selective epoxide hydrolase [Mus musculus]	803	0.0	G
gb ABU95055.1 epoxide hydrolase 2C [Mus musculus]	791	0.0	G
ref XP_001330051.1 PREDICTED: similar to soluble epoxide hyd...	717	0.0	UG
ref NP_001006712.1 epoxide hydrolase 2, cytoplasmic [Xenopus...	677	0.0	UG
ref NP_001006717.1 epoxide hydrolase 2, cytoplasmic [Gallus ...	675	0.0	UG
ref NP_001006717.1 epoxide hydrolase 2, cytoplasmic [Xenopus...	669	0.0	UG
emb CAH91370.1 hypothetical protein [Pongo pygmaeus]	644	0.0	
ref XP_001521600.1 PREDICTED: similar to epoxide hydrolase 2...	612	3e-173	UG
ref NP_001008642.1 epoxide hydrolase 2, cytoplasmic [Danio r...	572	2e-161	UG
emb CAG00866.1 unnamed protein product [Tetraodon nigroviridis]	479	4e-133	
gb EAW63550.1 epoxide hydrolase 2, cytoplasmic, isoform CRA_...	463	1e-128	G
ref XP_725168.2 PREDICTED: similar to Ephx2-prov protein [St...	454	8e-126	UG
ref XP_001164789.1 PREDICTED: similar to Ephx2-prov protein ...	448	3e-124	UG
ref XP_001190554.1 PREDICTED: similar to Ephx2-prov protein ...	420	1e-115	UG
ref XP_725076.2 PREDICTED: similar to Ephx2-prov protein, pa...	420	2e-115	UG
ref XP_001641873.1 predicted protein [Nematostella vectensis...	404	1e-110	G
ref XP_001191957.1 PREDICTED: similar to soluble epoxide hyd...	309	4e-82	UG
ref XP_001253507.1 PREDICTED: hypothetical protein [Bos taurus]	284	1e-74	UG
ref NP_767754.1 epoxide hydrolase [Bradyrhizobium japonicum ...	236	4e-60	G
ref YP_486290.1 Alpha/beta hydrolase [Rhodopseudomonas palus...	235	6e-60	G
ref YP_001413763.1 alpha/beta hydrolase fold [Parvibaculum l...	234	1e-59	G
ref XP_001179641.1 PREDICTED: similar to soluble epoxide hyd...	234	1e-59	UG
ref NP_120043.1 epoxide hydrolase [Caulobacter crescentus CB...	232	5e-59	G
ref XP_001683339.1 alpha/beta hydrolase fold [Caulobacter sp...	231	1e-58	G
ref YP_761108.1 putative epoxide hydrolase [Hyphomonas neptu...	227	2e-57	G
ref NP_821315.1 epoxide hydrolase [Streptomyces avermitilis ...	223	3e-56	G
ref YP_562843.1 alpha/beta hydrolase fold [Rhodopseudomonas ...	223	4e-56	G

gb E0147179.1	epoxide hydrolase 2, cytoplasmic, isoform CRA_...	204	4e-56	G
ref NP_219174.1	PROBABLE EPOXIDE HYDROLASE EPHA (EPOXIDE HYD...	202	7e-56	G
ref YP_001210928.1	alpha/beta hydrolase fold [Clostridium be...	219	3e-55	G
ref YP_001853477.1	epoxide hydrolase Epha [Mycobacterium mar...	218	8e-55	G
ref YP_007699.1	epoxide hydrolase Epha [Mycobacterium ulcera...	218	8e-55	G
ref NP_771160.1	epoxide hydrolase [Bradyrhizobium japonicum ...	216	1e-54	G
ref YP_029896.1	putative epoxide hydrolase [Myxococcus xanth...	217	2e-54	G
ref NP_959380.1	Epha [Mycobacterium avium subsp. paratubercu...	217	2e-54	G
ref ZF_00877473.1	COG0596: Predicted hydrolases or acyltrans...	216	3e-54	
ref ZF_02299346.1	alpha/beta hydrolase fold [Rhodopseudomona...	216	4e-54	
ref NP_354796.1	epoxide hydrolase [Agrobacterium tumefaciens...	216	5e-54	G
ref YP_079919.1	hydrolase, alpha/beta fold family protein (M...	215	6e-54	G
ref NP_027771.1	epoxide hydrolase [Streptomyces coelicolor A...	215	9e-54	G
ref YP_001701281.1	Probable epoxide hydrolase Epha [Mycobact...	214	1e-53	G
ref YP_001240076.1	Putative epoxide hydrolase [Bradyrhizobiu...	214	1e-53	G
ref NP_949116.1	epoxide hydrolase [Rhodopseudomonas palustri...	214	2e-53	G
ref YP_001238693.1	putative epoxide hydrolase [Bradyrhizobiu...	217	3e-53	G
ref NP_326951.2	epoxide hydrolase [Agrobacterium tumefaciens...	213	4e-53	G
emb CAC44404.1	putative epoxide hydrolase [Streptomyces rimo...	209	3e-52	
ref ZF_01864412.1	putative epoxide hydrolase [Erythrobacter ...	209	4e-52	
ref YP_001244572.1	putative epoxide hydrolase [Bradyrhizobiu...	209	4e-52	G
ref ZF_01712897.1	probable epha protein-Mycobacterium tuberc...	209	6e-52	
ref YP_569556.1	alpha/beta hydrolase fold [Rhodopseudomonas ...	204	2e-50	G
gb ABK21215.1	unknown [Picea sitchensis]	202	3e-50	
ref NP_769521.1	epoxide hydrolase [Bradyrhizobium japonicum ...	202	6e-50	G
emb CAC44314.1	unnamed protein product [Vitis vinifera]	201	9e-50	
ref ZF_01507828.1	alpha/beta hydrolase fold [Burkholderia ph...	200	2e-49	
ref ZF_01616404.1	epoxide hydrolase [marine gamma proteobact...	200	2e-49	
ref YP_652156.1	hydrolase, alpha/beta fold family [Alcanivor...	199	4e-49	G
ref YP_791780.1	alpha/beta hydrolase fold [Rhodopseudomonas ...	199	4e-49	G
ref YP_260035.1	epha [Pseudomonas fluorescens Pf-5] >gb AA9...	199	5e-49	G
ref YP_001205815.1	epoxide hydrolase [Bradyrhizobium sp. ORS...	199	6e-49	G
gb ABL97491.1	putative epoxide hydrolase [uncultured marine ...	199	7e-49	
ref NP_824987.1	epoxide hydrolase [Streptomyces avermitilis ...	199	7e-49	G
ref YE_703564.1	probable epoxide hydrolase [Rhodococcus sp. ...	199	9e-49	G
ref YP_890327.1	epoxide hydrolase [Mycobacterium smegmatis s...	198	1e-48	G
dbj BAD13534.1	soluble epoxide hydrolase [Citrus jambhiri]	199	1e-48	
ref NP_823081.1	epoxide hydrolase [Streptomyces avermitilis ...	197	1e-48	G
ref YP_00107142.1	alpha/beta hydrolase fold [Mycobacterium ...	197	2e-48	G
ref NP_014921.1	alpha/beta hydrolase fold [Caulobacter sp...	196	3e-48	G
ref YP_041941.1	alpha/beta hydrolase fold [Mycobacterium sp....	196	4e-48	G
prf 11802377A	epoxide hydrolase	195	8e-48	
gb ABN03020.1	Epoxide hydrolase [Medicago truncatula]	194	2e-47	
gb ABL97724.1	epoxide hydrolase [uncultured marine bacterium...	194	2e-47	

Alignments

```

>gb|AAG14968.1|AF233336_1 G soluble epoxide hydrolase [Homo sapiens]
Length=556

  GENE ID: 2053 EPHX2 | epoxide hydrolase 2, cytoplasmic [Homo sapiens]
(Over 10 PubMed links)

Score = 1157 bits (2994), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 556/556 (100%), Positives = 556/556 (100%), Gaps = 0/556 (0%)

Query 1  MTLRAAVFDLDGVLALPAVFGVLGRTEELALPRGLLNDAFQKGGPEGATTRLMKGEITL 60
Sbjct 1  MTLRAAVFDLDGVLALPAVFGVLGRTEELALPRGLLNDAFQKGGPEGATTRLMKGEITL 60

Query 61  SQWIPLMEENCRKCSETAKVCLPKNFSEIKEIFDKAISARKINRPMLQAALMLRKKGFTTA 120
Sbjct 61  SQWIPLMEENCRKCSETAKVCLPKNFSEIKEIFDKAISARKINRPMLQAALMLRKKGFTTA 120

Query 121  ILTNTWLDDRAERDGLAQLMCELKMHFDLIESCQVGMVKPEPQIYKFLDLTKASPSEV 180
Sbjct 121  ILTNTWLDDRAERDGLAQLMCELKMHFDLIESCQVGMVKPEPQIYKFLDLTKASPSEV 180

Query 181  VFLDDIGANLKPARDLGMVTILVQDTDLTALKELEKVTGIQLLNTAPAPLPTSCNPDSMSHG 240
Sbjct 181  VFLDDIGANLKPARDLGMVTILVQDTDLTALKELEKVTGIQLLNTAPAPLPTSCNPDSMSHG 240

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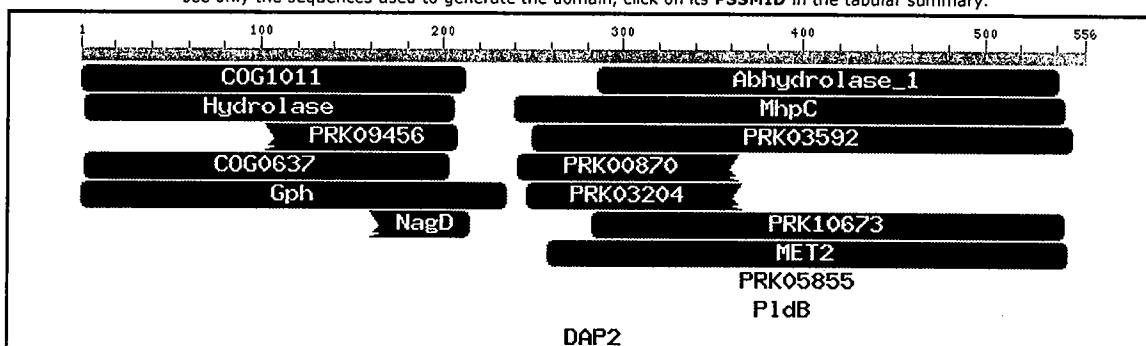
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Query sequence: [(local sequence)|cl|18838]

☐ Concise Result ☒ Full Result ☐ Show Search Information

Click on the **colored bar** for a conserved domain to **view your query sequence** within the multiple sequence alignment for that domain. To see only the sequences used to generate the domain, click on its **PSSMID** in the tabular summary.



Descriptions

	Title	PssmId	Multi-Dom	E-value
→	[+] pfam00561 , Abhydrolase_1, alpha/beta hydrolase fold. This catalytic domain is found in...	84863	No	2e-34
	[+] COG0596 , MhpC, Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfam...	30941	No	4e-27
	[+] PRK03592 , PRK03592 , haloalkane dehalogenase.	81168	No	8e-25
	[+] PRK00870 , PRK00870 , haloalkane dehalogenase.	80766	No	2e-18
→	[+] COG1011 , COG1011 , Predicted hydrolase (HAD superfamily) [General function prediction o...	31215	No	2e-14
	[+] pfam00702 , Hydrolase, haloacid dehalogenase-like hydrolase. This family are structural...	84963	No	2e-13
	[+] PRK03204 , PRK03204 , haloalkane dehalogenase.	81112	No	4e-13
	[+] PRK09456 , PRK09456 , phosphatase.	83014	No	3e-11
	[+] PRK10673 , PRK10673 , hypothetical protein.	83396	No	2e-07
	[+] COG0637 , COG0637 , Predicted phosphatase/phosphohexomutase [General function prediction...	30982	No	2e-07
	[+] COG0546 , Gph, Predicted phosphatases [General function prediction only].	30892	No	5e-06
	[+] COG2021 , MET2, Homoserine acetyltransferase [Amino acid transport and metabolism].	32204	No	8e-05
	[+] COG0647 , NagD, Predicted sugar phosphatases of the HAD superfamily [Carbohydrate trans...	30992	No	0.001
	[+] PRK05855 , PRK05855 , short chain dehydrogenase.	81768	Yes	1e-17
	[+] COG2267 , P1dB, Lysophospholipase [Lipid metabolism].	32448	Yes	1e-08
	[+] COG1506 , DAP2, Dipeptidyl aminopeptidases/acylaminoacyl-peptidases [Amino acid transpo...	31695	Yes	5e-05

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CD Search Reference:

Marchler-Bauer A, Bryant SH (2004), "CD-Search: protein domain annotations on the fly.", *Nucleic Acids Res.*32(W)327-331.

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BLAST Basic Local Alignment Search Tool

Job Title: human renin BLAST

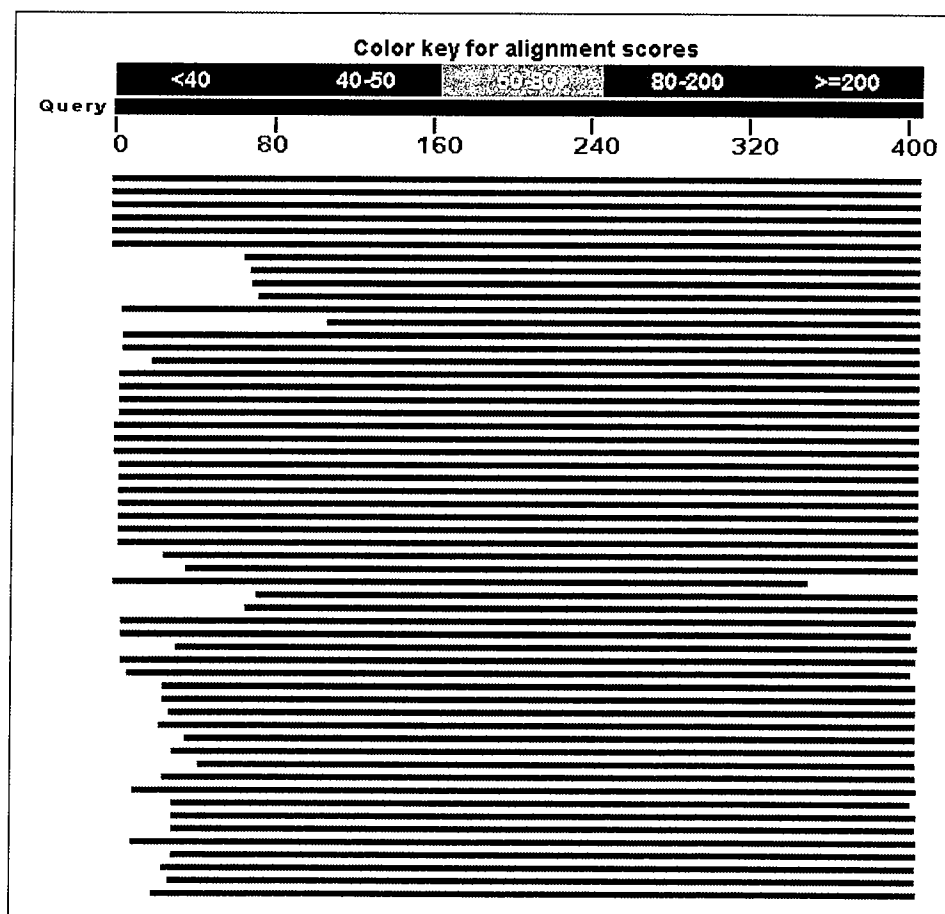
Show Conserved Domains

Putative conserved domains have been detected, click on the image below for detailed results.

**BLASTP 2.2.18 (Mar-02-2008)**

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402. Reference for compositional score matrix adjustment: Altschul, Stephen F., John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109. RID: 19U49KAP012
Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects 6,470,629 sequences; 2,208,486,882 total letters

Query= Length=406

Distribution of 100 Blast Hits on the Query Sequence

Distance tree of results **NEW** Related Structures

Sequences producing significant alignments:		Score (Bits)	E Value	
ref NP_000528.1	renin precursor [Homo sapiens] >ref NP_00100...	941	0.0	UG
sp Q6DLW5 RENI_MA...	Renin precursor (Angiotensinogenase) >gb...	838	0.0	
ref NP_001005995.1	renin [Macaca mulatta] >sp Q6DLW5 RENI_MA...	832	0.0	UG
gb EAW91505.1	renin [Homo sapiens] >gb EAW91505.1 renin [Ho...	807	0.0	G
gb AAA40304.1	renin	801	0.0	G
sp Q9T3Z1 RENI_CALDA	Renin precursor (Angiotensinogenase) >em...	773	0.0	
pdb 2BFS A	Chain A, Crystal Structure Of Renin-Pf00074777 Com...	701	0.0	S
pdb 1HRU A	Chain A, High Resolution Crystal Structures Of Rec...	696	0.0	S
pdb 2I4Q A	Chain A, Human ReninPF02342674 COMPLEX >pdb 2I4Q B...	694	0.0	S
pdb 2G24 A	Chain A, Ketopiperazine-Based Renin Inhibitors: Op...	688	0.0	S
ref NP_001001194.1	renin [Canis lupus familiaris] >sp Q6DYE7...	621	3e-176	UG
emb CAA24937.1	unnamed protein product [Homo sapiens]	615	3e-174	G
ref XP_001483754.1	PREDICTED: similar to preprorenin [Equus ...	614	3e-174	UG
ref XP_589249.3	PREDICTED: similar to renin [Bos taurus]	612	2e-173	UG
ref NP_001009299.1	renin [Ovis aries] >sp P52115 RENI_SHEEP ...	596	1e-168	UG
ref XP_001472702.1	PREDICTED: similar to renin 2 tandem dupl...	586	1e-165	UG
ref NP_112469.1	renin 1 structural [Mus musculus] >sp P06281...	580	9e-164	UG
gb A4440043.1	renin (Ren-1-d) >gb EDL01155.1 mCG129412 [Mus...	579	1e-163	G
ref XP_001472692.1	PREDICTED: similar to renin 2 tandem dupl...	578	2e-163	G
ref NP_036774.1	renin 1 [Rattus norvegicus] >sp P08424 RENI_...	574	4e-162	UG
gb AAA42936.1	preprorenin (EC 3.4.99.19)	572	1e-161	G
emb CAA30082.1	unnamed protein product [Rattus norvegicus]	572	2e-161	G
gb AAM61957.1	synthetic renin 2/1d [Mus musculus]	570	8e-161	
gb EDL01218.1	mCG6933 [Mus musculus]	566	1e-159	
sp P00796 RENI2_MOUSE	Renin-2 precursor (Angiotensinogenase) ...	565	3e-159	G
ref NP_112470.2	renin 2 tandem duplication of Ren1 [Mus musc...	564	4e-159	UG
gb AAH11473.1	Ren2 protein [Mus musculus]	563	9e-159	G
prf 08672832	renin precursor	560	8e-158	
gb AAA40050.1	renin [Mus musculus]	559	1e-157	G
emb CAA25381.1	renin [Mus musculus]	544	6e-153	G
gb EDM09771.1	renin 1, isoform CRA_a [Rattus norvegicus]	526	9e-148	G
gb AAA42031.1	renin	490	6e-137	G
pdb 1SMR A	Chain A, The 3-D Structure Of Mouse Submaxillary R...	488	2e-136	S
prf 11004236A	renin	485	3e-135	
ref XP_001370729.1	PREDICTED: similar to preprorenin [Monode...	464	4e-129	UG
emb CAJ55261.1	renin-like aspartic protease [Echis ocellatus]	446	1e-123	
ref XP_001320972.1	PREDICTED: similar to preprorenin [Ornith...	429	2e-118	UG
ref XP_001370701.1	PREDICTED: similar to preprorenin [Monode...	424	8e-117	G
emb CAJ55260.1	renin-like aspartic protease [Echis ocellatus]	413	1e-113	
ref NP_998025.1	renin [Danio rerio] >gb AAO31713.1 renin pr...	401	5e-110	UG
gb AAO41706.1	renin precursor [Danio rerio] >emb CAQ13643.1 ...	400	1e-109	G
emb CAG11313.1	unnamed protein product [Tetraodon nigroviridis]	396	1e-108	
ref NP_001073054.1	renin [Takifugu rubripes] >tpg DAA01803.1...	395	4e-108	UG
ref XP_001370755.1	PREDICTED: similar to renin [Monodelphis ...	393	1e-107	G
ref XP_001370599.1	PREDICTED: similar to preprorenin [Monode...	382	4e-104	G
ref XP_001372231.1	PREDICTED: similar to preprorenin [Monode...	379	3e-103	G
ref XP_966517.1	PREDICTED: similar to CG1548-PA isoform 1 [T...	356	2e-96	UG
ref NP_001072052.1	cathepsin D1 [Takifugu rubripes] >dbj BAD...	355	3e-96	UG
sp Q9DEX3 CATD_CLUHA	Cathepsin D precursor >gb AAG27733.1 AF3...	352	4e-95	
ref NP_001085403.1	MGC82347 protein [Xenopus laevis] >gb AAH...	352	4e-95	UG
gb AAM62293.1 AF396662_1	cathepsin D preproprotein [Silurus a...	349	2e-94	
gb AAH42316.1	Ctsd protein [Danio rerio] >gb AAH62824.1 Cts...	349	2e-94	G
gb AAL61540.1	cathepsin D precursor [Danio rerio]	349	3e-94	G
ref XP_975746.1	PREDICTED: similar to CG1548-PA isoform 2 [T...	348	4e-94	UG
ref XP_001641225.1	predicted protein [Nematostella vectensis...	347	7e-94	G

gb A6V59077.1	cathepsin D [Lates calcarifer]	347	7e-94	
ref XP_975626.1	PREDICTED: similar to CG1548-PA isoform 3 [T...	347	7e-94	UG
emb CAF91576.1	unnamed protein product [Tetraodon nigroviridis]	347	7e-94	
emb CAK11131.1	cathepsin D [Danio rerio] >emb CAK05390.1 ca...	347	8e-94	G
ref NP_001005701.1	cathepsin D (lysosomal aspartyl protease)...	346	2e-93	UG
ref NP_990509.1	cathepsin D [Gallus gallus] >sp Q05744 CATD_...	346	2e-93	UG
gb AAC60301.1	cathepsin D [Oncorhynchus mykiss]	344	6e-93	G
ref NP_571785.1	cathepsin D [Danio rerio] >emb CAC20111.1 c...	342	4e-92	UG
ref XP_001332443.1	PREDICTED: hypothetical protein [Danio re...	341	6e-92	UG
gb AAD03419.1	cathepsin D; lysosomal aspartic proteinase [Hy...	341	6e-92	
gb ARI95390.1	cathepsin D [Hippoglossus hippoglossus]	341	7e-92	
emb CAA08878.1	Cathepsin D [Podarcis sicula]	341	7e-92	
ref XP_001091374.1	PREDICTED: cathepsin D isoform 1 [Macaca ...	340	9e-92	UG
ref NP_906325.1	hypothetical protein LOC336746 [Danio rerio]...	340	1e-91	UG
gb AAI54878.1	Unknown (protein for MGC:180677) [Xenopus trop...	340	1e-91	
gb AAT23963.1	LOC613063 protein [Xenopus tropicalis]	340	2e-91	G
gb AAH96030.1	LOC613063 protein [Xenopus tropicalis]	339	2e-91	G
sp Q93426 CATD_CHINA	Cathepsin D precursor	339	3e-91	
ref XP_392857.2	PREDICTED: similar to cathD CG1548-PA [Apis ...	339	4e-91	UG
ref XP_307784.1	AGAP003277-PA [Anopheles gambiae str. PEST] ...	339	4e-91	UG
ref NP_001093565.1	hypothetical protein LOC398994 [Xenopus l...	339	5e-91	UG
emb CAH50861.1	hypothetical protein [Pongo pygmaeus]	337	7e-91	
gb ABX52210.1	cathepsin D (predicted) [Papio anubis]	337	9e-91	G
gb ACB21270.1	cathepsin D preproprotein (predicted) [Callice...	337	1e-90	
ref NP_001085309.1	hypothetical protein LOC443721 [Xenopus l...	336	1e-90	UG
ref XP_001091601.1	PREDICTED: cathepsin D isoform 3 [Macaca ...	336	2e-90	UG
gb AAH75134.1	LOC443721 protein [Xenopus laevis]	336	2e-90	G
dbj BAE87520.1	unnamed protein product [Macaca fascicularis]	335	3e-90	
ref XP_001091495.1	PREDICTED: cathepsin D isoform 2 [Macaca ...	335	3e-90	UG
gb ABM64473.1	cathepsin D (lysosomal aspartyl peptidase) [sy...	335	5e-90	G
gb AAK29797.1	cathepsin D [synthetic construct]	334	7e-90	
gb AAK236524.1	cathepsin D [synthetic construct] >gb AAX42359...	334	7e-90	
gb AAI19630.1	Homo sapiens cathepsin D (lysosomal aspartyl p...	334	8e-90	
ref NP_001490.1	cathepsin D preproprotein [Homo sapiens] >sp...	334	8e-90	UG
ref NP_001006172.1	MGC89016 protein [Xenopus tropicalis] >gb...	332	3e-89	UG
gb AAV90625.1	cathepsin D protein [Sus scrofa]	332	4e-89	G
gb ACC68942.1	cathepsin D (predicted) [Rhinolophus ferrumequ...	332	5e-89	
ref NP_001020793.1	cathepsin D [Canis lupus familiaris] >sp ...	331	7e-89	UG
emb CAA07219.1	cathepsin D precursor [Chionodraco hamatus]	330	1e-88	
sp P24268 CATD_RAT	Cathepsin D precursor [Contains: Cathepsin...	330	1e-88	G
ref NP_529161.2	cathepsin D [Rattus norvegicus] >gb AAH62032...	329	2e-88	UG
ref NP_988964.1	cathepsin D (lysosomal aspartyl protease) [X...	329	2e-88	UG
ref XP_001600543.1	PREDICTED: similar to GA13759-PA [Nasonia...	328	3e-88	G
dbj BAE30902.1	unnamed protein product [Mus musculus]	328	5e-88	G
ref NP_001032810.1	cathepsin D [Sus scrofa] >gb AAY42144.1 ...	328	6e-88	UG

Alignments

```

>ref|NP_000528.1| UG renin precursor [Homo sapiens]
ref|NP_001009122.1| UG renin [Pan troglodytes]
sp|P00797|RENI_HUMAN G Renin precursor (Angiotensinogenase)
sp|P60016|RENI_PANTR G Renin precursor (Angiotensinogenase)
gb|AAG30305.1|AF193456_1 G renin [Pan troglodytes]
gb|AAA60363.1| G renin [Homo sapiens]
gb|AAD03461.1| G renin [Homo sapiens]
gb|AAH47752.1| G Renin [Homo sapiens]
emb|CAG38737.1| G REN [Homo sapiens]
gb|AAH33474.1| G Renin [Homo sapiens]

```



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	Title	PssmId	Multi-Dom	E-value
[+]pfam00026	Asp, Eukaryotic aspartyl protease. Aspartyl (acid) proteases include pepsin...	84452	No	1e-104
[+]pfam07966	A1_Propeptide, A1 Propeptide. Most eukaryotic endopeptidases (Merops Family...	87413	No	0.004

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CD Search Reference:

Marchler-Bauer A, Bryant SH (2004), "CD-Search: protein domain annotations on the fly.", *Nucleic Acids Res.*32(W)327-331.

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